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RAW SEQUENCE LISTING

DATE: 11/28/2001

PATENT APPLICATION: US/09/922,683

TIME: 10:38:37

Input Set : N:\Crf3\RULE60\09922683.txt

Output Set: N:\CRF3\11282001\I922683.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: DECKER, Heinrich

8 (ii) TITLE OF INVENTION: ISOLATION OF THE BIOSYNTHESIS GENES FOR

9 PSEUDO-OLIGOSACCHARIDES FROM STREPTOMYCES GLAUDESCENS

10 GLA. O AND THEIR USE

12 (iii) NUMBER OF SEQUENCES: 13

14 (iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: FOLEY & LARDNER

16 (B) STREET: 3000 K Street, N.W.

17 (C) CITY: Washington

18 (D) STATE: D.C.

19 (E) COUNTRY: U.S.A.

20 (F) ZIP: 20007-5109

22 (v) COMPUTER READABLE FORM:

23 (A) MEDIUM TYPE: Floppy disk

24 (B) COMPUTER: IBM PC compatible

25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

28 (vi) CURRENT APPLICATION DATA:

C--> 29 (A) APPLICATION NUMBER: US/09/922,683

C--> 30 (B) FILING DATE: 07-Aug-2001

31 (C) CLASSIFICATION:

37 (vii) PRIOR APPLICATION DATA:

34 (A) APPLICATION NUMBER: 09/194,905

35 (B) FILING DATE: 1999-12-01

38 (A) APPLICATION NUMBER: DE 19622783.6

39 (B) FILING DATE: 07-JUN-1996

41 (viii) ATTORNEY/AGENT INFORMATION:

42 (A) NAME: Granados, Patricia D.

43 (B) REGISTRATION NUMBER: 33,683

44 (C) REFERENCE/DOCKET NUMBER: 026083/0193

46 (ix) TELECOMMUNICATION INFORMATION:

47 (A) TELEPHONE: (202) 672-5300

48 (B) TELEFAX: (202) 672-5399

51 (2) INFORMATION FOR SEQ ID NO: 1:

53 (i) SEQUENCE CHARACTERISTICS:

54 (A) LENGTH: 22 base pairs

55 (B) TYPE: nucleic acid

56 (C) STRANDEDNESS: single

57 (D) TOPOLOGY: linear

59 (ii) MOLECULE TYPE: other nucleic acid

60 (A) DESCRIPTION: /desc = "Primer"

65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

67 CSGGSGSSGC SGGSTTCATS GG

69 (2) INFORMATION FOR SEQ ID NO: 2:

71 (i) SEQUENCE CHARACTERISTICS:

ENTERED

22

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72      (A) LENGTH: 24 base pairs
73      (B) TYPE: nucleic acid
74      (C) STRANDEDNESS: single
75      (D) TOPOLOGY: linear
77      (ii) MOLECULE TYPE: other nucleic acid
78      (A) DESCRIPTION: /desc = "Primer"
83      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
85 GGGWVCTGGY VSGGSCCGTA GTTG                                     24
87 (2) INFORMATION FOR SEQ ID NO: 3:
89      (i) SEQUENCE CHARACTERISTICS:
90          (A) LENGTH: 546 base pairs
91          (B) TYPE: nucleic acid
92          (C) STRANDEDNESS: single
93          (D) TOPOLOGY: linear
95      (ii) MOLECULE TYPE: DNA (genomic)
100     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
102 CCCGGGCGGG GCGGGGTCA TCGGCTCCGC CTACGTCCGC CGGCTCCTGT CGCCCGGGGC      60
104 CCCCGGCGGC GTCGCGGTGA CCGTCTCGA CAAACTCACC TACGCCGGA GCCTCGCCCG      120
106 CCTGCACGCG GTGCGTGACC ATCCCGCCT CACCTTCGTC CAGGGCGACG TGTGCGACAC      180
108 CGCGCTCGTC GACACGCTGG CCGCGCGGCA CGACGACATC GTGCACTTCG CGGCCGAGTC      240
110 GCACGTCGAC CGTCCATCA CCGACAGCGG TGCCTTCACC CGCACCAACG TGCTGGGCAC      300
112 CCAGGTCCTG CTCGACGCCG CGTCCGCCA CGGTGTGCGC ACCCTCGTGC ACGTCTCCAC      360
114 CGACGAGGTG TACGGCTCCC TCCCGCACGG GGCCGCCGCG GAGAGCGACC CCCTGCTCCC      420
116 GACCTCGCCG TACGCGGCGT CGAAGGCGGC CTCGGACCTC ATGGCGCTCG CCCACCACCG      480
118 CACCACGGC CTGGACGTCC GGGTGACCCG CTGTTCGAAC AACTACGGCC CGCACCAGTT      540
120 CCCGGG                                     546
122 (2) INFORMATION FOR SEQ ID NO: 4:
124     (i) SEQUENCE CHARACTERISTICS:
125         (A) LENGTH: 541 base pairs
126         (B) TYPE: nucleic acid
127         (C) STRANDEDNESS: single
128         (D) TOPOLOGY: linear
130     (ii) MOLECULE TYPE: DNA (genomic)
135     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
137 CCCCGGGTGC TGGTAGGGGC CGTAGTTGTT GGAGCAGCGG GTGATGCGCA CGTCCAGGCC      60
139 GTGGCTGACG TGCATGGCCA GCGCGAGCAG GTCGCCCCGAC GCCTTGAGAG TGGCATAGGG      120
141 GCTGTTGGGG CGCAGCGGCT CGTCTCCCGT CCACGACCCC GTCTCCAGCG AGCCGTAGAC      180
143 CTCGTCGGTG GACACCTGCA CGAAGGGGGC CACGCCGTGC CGCAGGGCCG CGTCGAGGAG      240
145 TGTCTGCGTG CCGCCGGCGT TGGTCCGCAC GAACGCGGCG GCATCGAGCA GCGAGCGGTC      300
147 CACGTGCGAC TCGGCGGCGA GGTGCACGAC CTGGTCTTGG CCGGCCATGA CCCGGTCGAC      360
149 CAGGTCCGCG TCGCAGATGT CGCCGTGGAC GAAGCGCAGC CGGGGGTGGT CGCGGACCGG      420
151 GTCGAGGTTG GCGAGGTTGC CGGCGTAGCT CAGGGCGTCG AGCACGGTGA CGACGGCGTC      480
153 GGGCGGCCCG TCCGACCGA GGAGGGTGCG GACGTAGTGC GAGCCCATGA ACCCGCCCGC      540
155 C                                     541
157 (2) INFORMATION FOR SEQ ID NO: 5:
159     (i) SEQUENCE CHARACTERISTICS:
160         (A) LENGTH: 180 amino acids
161         (B) TYPE: amino acid
162         (C) STRANDEDNESS:

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163         (D) TOPOLOGY: linear
165     (ii) MOLECULE TYPE: protein
170     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
172     Ala Ala Gly Phe Met Gly Ser His Tyr Val Arg Thr Leu Leu Gly Pro
173     1             5             10             15
175     Asp Gly Pro Pro Asp Ala Val Val Thr Val Leu Asp Ala Leu Ser Tyr
176     20             25             30
178     Ala Gly Asn Leu Ala Asn Leu Asp Pro Val Arg Asp His Pro Arg Leu
179     35             40             45
181     Arg Phe Val His Gly Asp Ile Cys Asp Ala Asp Leu Val Asp Arg Val
182     50             55             60
184     Met Ala Gly Gln Asp Gln Val Val His Leu Ala Ala Glu Ser His Val
185     65             70             75             80
187     Asp Arg Ser Leu Leu Asp Ala Ala Ala Phe Val Arg Thr Asn Ala Gly
188     85             90             95
190     Gly Thr Gln Thr Leu Leu Asp Ala Ala Leu Arg His Gly Val Ala Pro
191     100            105            110
193     Phe Val Gln Val Ser Thr Asp Glu Val Tyr Gly Ser Leu Glu Thr Gly
194     115            120            125
196     Ser Trp Thr Glu Asp Glu Pro Leu Arg Pro Asn Ser Pro Tyr Ala Thr
197     130            135            140
199     Ser Lys Ala Ser Gly Asp Leu Leu Ala Leu Ala Met His Val Ser His
200     145            150            155            160
202     Gly Leu Asp Val Arg Ile Thr Arg Cys Ser Asn Asn Tyr Gly Pro Tyr
203     165            170            175
205     Gln His Pro Gly
206     180
208 (2) INFORMATION FOR SEQ ID NO: 6:
210     (i) SEQUENCE CHARACTERISTICS:
211         (A) LENGTH: 181 amino acids
212         (B) TYPE: amino acid
213         (C) STRANDEDNESS:
214         (D) TOPOLOGY: linear
216     (ii) MOLECULE TYPE: protein
221     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
223     Pro Gly Gly Ala Gly Phe Ile Gly Ser Ala Tyr Val Arg Arg Leu Leu
224     1             5             10             15
226     Ser Pro Gly Ala Pro Gly Gly Val Ala Val Thr Val Leu Asp Lys Leu
227     20             25             30
229     Thr Tyr Ala Gly Ser Leu Ala Arg Leu His Ala Val Arg Asp His Pro
230     35             40             45
232     Gly Leu Thr Phe Val Gln Gly Asp Val Cys Asp Thr Ala Leu Val Asp
233     50             55             60
235     Thr Leu Ala Ala Arg His Asp Asp Ile Val His Phe Ala Ala Glu Ser
236     65             70             75             80
238     His Val Asp Arg Ser Ile Thr Asp Ser Gly Ala Phe Thr Arg Thr Asn
239     85             90             95
241     Val Leu Gly Thr Gln Val Leu Leu Asp Ala Ala Leu Arg His Gly Val
242     100            105            110

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244   Arg Thr Leu Val His Val Ser Thr Asp Glu Val Tyr Gly Ser Leu Pro
245           115                      120                      125
247   His Gly Ala Ala Ala Glu Ser Asp Pro Leu Leu Pro Thr Ser Pro Tyr
248           130                      135                      140
250   Ala Ala Ser Lys Ala Ala Ser Asp Leu Met Ala Leu Ala His His Arg
251           145                      150                      155                      160
253   Thr His Gly Leu Asp Val Arg Val Thr Arg Cys Ser Asn Asn Tyr Gly
254           165                      170                      175
256   Pro His Gln Phe Pro
257           180
259 (2) INFORMATION FOR SEQ ID NO: 7:
261     (i) SEQUENCE CHARACTERISTICS:
262         (A) LENGTH: 6854 base pairs
263         (B) TYPE: nucleic acid
264         (C) STRANDEDNESS: single
265         (D) TOPOLOGY: linear
267     (ii) MOLECULE TYPE: DNA (genomic)
272     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
274 CTGCAGGGTT CCCTGGTGCA CGACCCGCCC CTGGTTCGACG ACCAGGGGCGC TGTCGCAGAT      60
276 CGCGGCGATG TCGGCGATGT CGTGGCTGGT GAGCACCACG GTGGTGCCCA GTTCCCGGTG      120
278 GGCGCGGTTG ACCAGCCGGC GCACCGCGTC CTTCAGCACC ATGTCGAGGC CGATCGTGGG      180
280 CTCGTCCAG AACAGCACGG CCGGGTCGTG CAGCAGGCTC GCCGCGATCT CGGCGCGCAT      240
282 GCGCTGTCCG AGGCTGAGCT GCCGCACGGG GGTGGACCCC AGCGCGTCGA TGTCGAGGAG      300
284 GTCCCGGAAC AGGGCGAGGT TGCGCCGGTA GACCGGTCCG GGGATGTCTGT AGATGCGGCG      360
286 CAGGATGCGG AAGGAGTCGG GTACCGACAG GTCCCACCAG AGCTGGCTGC GCTGGCCGAA      420
288 GACGACCGCG ATCGTGCGGG CGTTGCGCTG CCGGTGCCGG TAGGGCTCCA GCCCGGCGAC      480
290 CGTGCAGCGG CCGGAGGTGG GGGTCATGAT GCCGGTCAGC ATCTTGATCG TGGTGCAGTT      540
292 GCCGGCTCCG TTGGCGCCGA TGTAGGCGGT CTTCGTGCCG GCCGGTATCT CGAAGGAGAC      600
294 GTCGTCGACG GCGCGCACGA CGCGGTACCG GCGGGTCAGG AGGGTGGAGA GGCTGCCGAG      660
296 CAGGCCGGGC TCGCGTTCGG CCAGCCGGAA CTCCTTGACG AGGTGTTTCG CCACGATCAC      720
298 GCGATCACCC GCTCGACGGC CGTCTCCAGC AGGCGCAGGC CCTCGTCGAG CAGCGCCTCG      780
300 TCGAGGGTGA ACGGCGGTGC CAGCCGAGG ATGTGGCCGC CCAGGGAGGT GCGCAGCCCC      840
302 AGGTCGAGGG CGGTGGTGTA GACGGCCCCG GCGGTCTCGG GGGCGGGTGC CCGGCCGACG      900
304 GCGTCGGTGA CGAACTCCAG GCCCCACAG AGTCCGAGG CGCGTACCTG GCCGAGCTGG      960
306 GGGAAGCGGG ACTCCAGGGC GCGCAGCCGC TCCTGGATGA GCTCGCCGAG GACGCGCACG      1020
308 CGGTCGATCA GCCGGTCGCG CTCGACGACC TCCAGCGTGG CGCGGGCGGC GGCGATCCCC      1080
310 AGTGGGTTGC TCGCGTACGT CGAGGCGTAC GCCCCGGGGT GGCCGCCTCC GGCCTGCGCA      1140
312 GCTTCCGCGC GTCCGGCCAG CACGGCGAAG GGGAATCCGC TCGCGGTGCC CTTGGACAGC      1200
314 ATCGCCAGGT CCGGCTCGAT GCCGAACAGT TCGCTGGCGA GGAAGGCGCC GGTGCGCCCC      1260
316 CCGCCGGTGA GGACCTCGTC GGCGACGAGC AGCAGCCGC CGTCCCGGCA GGCGCCGGCG      1320
318 ATCCGCTCCC AGTAGCCGGG GGGCGGCACG ATGACGCCTG CCGCGCCGAG GACGGGTTTC      1380
320 AAGACCAGGG CCGAGACGTT GGGCTTCTCC GCGATGTGCC GGCGCACGAG GGTGCGGCAC      1440
322 CGCACGTCGC ACGAGGGGTA CTCCAGGCCC AGGGGACAGC GGTAGCCAGT AGGGGCTGTA      1500
324 GCCAGCACGC TGTGCGCGCT GAAGGCCTGG TGGCCGATGT CCCAGTGGAC CAGCATCCGG      1560
326 GCGCCCATGG TCTTGCCGTG GAAGCCGTGG CGCAGGGCGC AGATCCGGTT GCGGCCCGGC      1620
328 GCGGCGGTGC CCTGGACGAC CCGCAGGGCG GCCTCGACCA CCTCCGCGCC GGTGGAGAAG      1680
330 AAGGCGTAGG TGTCGAGCTC TTCCGGCCAC ACCCTGGCCA GCAGTTCCAG CAGGCCGGCG      1740
332 CGGTCCGGCG TGGCGCTGTC GTGGACGTTT CACAGGCGGC GGGCCTGGGT GGTGAGTGCC      1800
334 TCGACGACCT CCGGGTGCCC GTGGCCAGT GACTGGGTGA GGGTCCCGGC CGCGAAGTCG      1860

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336	AGGTACTGGT	TGCCGTCCAG	GTCGGTCAGA	ACGGGACCGC	GTCCCTCGGC	GAAGACCCGG	1920
338	CGTCCGTGGA	CGGCTTCCTC	GGAGGCGCCC	GGCGCCAGGT	GGCGGGCCTC	CCGTGCCAGG	1980
340	TGCTGTGTCT	GCCGTAAGCC	TGTCATCGCT	GCCTCTGCTC	GTCGGACCGG	CTGACGCGAT	2040
342	CGCCGGCGAA	CTGCGTTGTG	GCGCACCACG	GTTGGGGCGG	CTCGGCGCTG	AGTCAAACAC	2100
344	TTGAACACAC	ACCCTGCAA	GAGTTTGCGG	GTTGTTTCAG	AAAGTTGTTG	CGAGCGGCCC	2160
346	CGGCACTCTG	GTTGAGTCGA	CGTGCTTACG	GCGCCACCAC	GCCTCACGTT	CGAGGAGGGA	2220
348	CCTGTGAGAA	CAAGCCCGCA	GACCGACCCG	CTCCCGCGGA	GGCCGAGGTG	AAGGCCCTGG	2280
350	TCCTGGCAGG	TGGAACCGGC	AGCAGACTGA	GGCCGTTTAC	CCACACCGCC	GCCAAGCAGC	2340
352	TGCTCCCAT	CGCCAACAAG	CCCGTGCTCT	TCTACGCGCT	GGAGTCCCTC	GCCGCGGCGG	2400
354	GTGTCCGGGA	GGCCGGCGTC	GTCGTGGGCG	CGTACGGCCG	GGAGATCCGC	GAACTCACCG	2460
356	GCGACGGCAC	CGCGTTCGGG	TTACGCATCA	CCTACCTCCA	CCAGCCCGCG	CCGCTCGGTC	2520
358	TCGCGCACGC	GGTGCGCATC	GCCC CGGGCT	TCCTGGGCGA	CGACGACTTC	CTGCTGTACC	2580
360	TGGGGGACAA	CTACCTGCCC	CAGGGCGTCA	CCGACTTCGC	CCGCCAATCG	GCCGCCGATC	2640
362	CCGCGGCGGC	CCGGCTGCTG	CTCACCCCGG	TCGCGGACCC	GTCCGCCTTC	GGCGTCGCGG	2700
364	AGGTCGACGC	GGACGGGAAC	GTGCTGCGCT	TGGAGGAGAA	ACCCGACGTC	CCGCGCAGCT	2760
366	CGCTCGCGCT	CATCGGCGTG	TACGCCTTCA	CCCCGCCCGT	CCACGAGGCG	GTACGGGCCA	2820
368	TCACCCCTC	CGCCCGCGGC	GAGCTGGAGA	TCACCCACGC	CGTGCAGTGG	ATGATCGACC	2880
370	GGGGCCTGCG	CGTACGGGCC	GAGACCACCA	CCCCGCCCTG	GCGCGACACC	GGCAGCGCGG	2940
372	AGGACATGCT	GGAGGTCAAC	CGTCACGTCC	TGGACGGA	GGAGGGCCGC	ATCGAGGGGA	3000
374	AGGTCGACGC	GCACAGCACG	CTGGTCGGCC	GGGTCCGGGT	GGCCGAAGGC	GCGATCGTGC	3060
376	GGGGGTACAA	CGTGGTGGGC	CCGGTGGTGA	TCGGCGCGGG	TGCCGTGCTC	AGCAACTCCA	3120
378	GTGTGCGCCC	GTACACCTCC	ATCGGGGAGG	ACTGCCGGGT	CGAGGACAGC	GCCATCGAGT	3180
380	ACTCCGTCCT	GCTGCGCGGC	GCCCAGGTCG	AGGGGGCGTC	CCGCATCGAG	GCGTCCCTCA	3240
382	TCGGCCGCGG	CGCCGTGCTC	GGCCCGGCCC	CCCGTCTCCC	GCAGGCTCAC	CGACTGGTGA	3300
384	TCGGCGACCA	CAGCAAGGTG	TATCTACCCC	CATGACCACG	ACCATCCTCG	TCACCGGCGG	3360
386	AGCGGGCTTC	ATTCGCTCCG	CCTACGTCCG	CCGGCTCCTG	TCGCCCCGGG	CCCCCGGCGG	3420
388	CGTCGCGGTG	ACCGTCCCTG	ACAAACTCAC	CTACGCCGGC	AGCCTCGCCC	GCCTGCACGC	3480
390	GGTGCGTGAC	CATCCCGGCC	TCACCTTCGT	CCAGGGCGAC	GTGTGCGACA	CCGCGCTCGT	3540
392	CGACACGCTG	GCCGCGCGGC	ACGACGACAT	CGTGCACTTC	GCGGCCGAGT	CGCACGTCTGA	3600
394	CCGCTCCATC	ACCACAGCG	GTGCCTTCAC	CCGCACCAAC	GTGCTGGGCA	CCCAGGTCTT	3660
396	GCTCGACGCC	GCGCTCCGCC	ACGGTGTGCG	CACCTTCGTG	CACGTCTCCA	CCGACGAGGT	3720
398	GTACGGCTCC	CTCCCGCACG	GGGCCGCCGC	GGAGAGCGAC	CCCCTGCTTC	CGACCTCGCC	3780
400	GTACGCGGCG	TCGAAGGCGG	CCTCGGACCT	CATGGCGCTC	GCCCACCACC	GCACCCACGG	3840
402	CCTGGACGTC	CGGGTGACCC	GCTGTTCGAA	CAACTTCGGC	CCCCACCAGC	ATCCCCGAGAA	3900
404	GCTCATACCG	CGCTTCCTGA	CCAGCCTCCT	GTCCGGCGGC	ACCGTTCCCC	TCTACGGCGA	3960
406	CGGGCGGCAC	GTGCGCGACT	GGCTGCACGT	CGACGACCAC	GTCAGGGCCG	TCGAACCTCGT	4020
408	CCGCGTGTCT	GGCCGGCCCG	GAGAGATCTA	CAACATCGGG	GGCGGCACCT	CGCTGCCCAA	4080
410	CCTGGAGCTC	ACGCACCGGT	TGCTCGCACT	GTGCGGCGCG	GGCCCGGAGC	GCATCGTCCA	4140
412	CGTCGAGAAC	CGCAAGGGGC	ACGACCGGCG	CTACGCGGTC	GACCACAGCA	AGATCACCGC	4200
414	GGAACCTCGT	TACCGGCCCG	GCACCGACTT	CGCGACCGCG	CTGGCCGACA	CCGCGAAGTG	4260
416	GTACGAGCGG	CACGAGGACT	GGTGGCGTCC	CCTGCTCGCC	GCGACATGAC	GTGCGGCGCG	4320
418	ACCGCAACCA	CCGGCCCCCG	CCGGCACACC	GCCGCCCGCG	GCCGGTGGCC	GGCCGGTCAG	4380
420	CGTCCGTGAG	CCGGGCGCCG	GCCGCCCGCG	GGGCCGGCGG	CGGTGGACCC	CCGACCACC	4440
422	AGTTCCGGCA	TGAAGACGAA	TTCCGTGCGC	GGCGGCGGCG	TTCCGCTCAT	CTCCTCCAGC	4500
424	AGTGCGTCCA	CGGCGACCTG	CCCCATCGCC	TTGACGGGCT	GTCTGATGGT	GGTCAGGGGA	4560
426	GGGTGCGTGA	AGGCCATGAG	CGGCGAGTCG	TCGAAGCCGA	CCACCGAGAT	GTCACCGGGA	4620
428	ACCGTGAGAC	CCCGCCGGCG	CGCGGCCCGC	ACGGCGCCCA	CGGCCATCAT	GTCGCTGGCG	4680
430	CACATGACGG	CGGTGCAGCC	CAGGTGCATC	AGCGCGGACG	CGGCGGCTTG	GCCCCCTTCC	4740
432	AGGGAGAACA	GCGAGTGCTG	CACGAGCTCC	TCGGACTCCC	GCGCCGACAC	TCCCAGGTGC	4800

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L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]